

Fig 1

Fig 1

Spacing Between Adjacent Peaks in the Raw Data
(M13, T's T=6%, 60C, Long Gel)

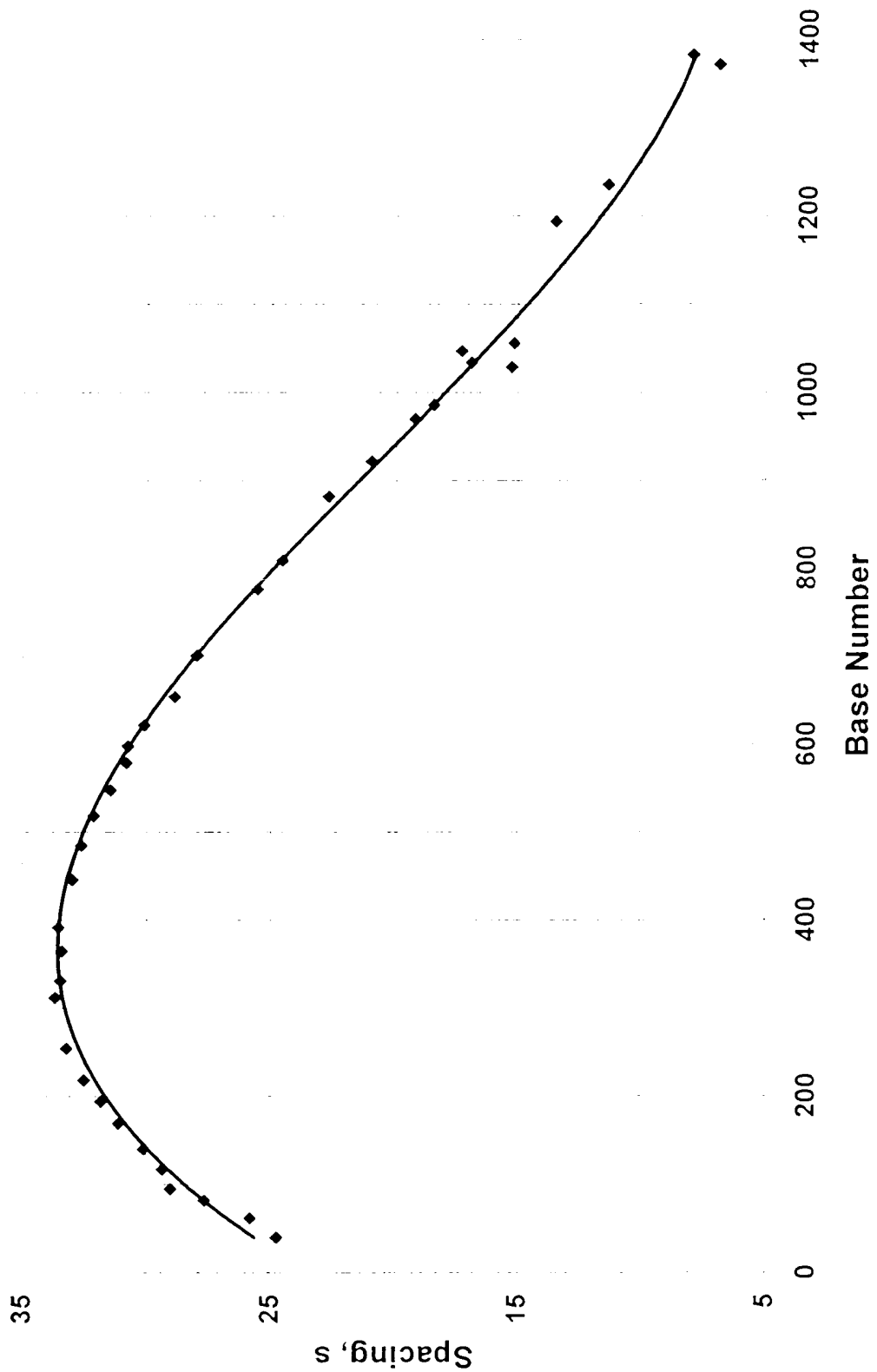


fig. 2

Spacing Between Adjacent Bases
(for Different Number of Peaks Used for Alignment of Raw Data)
(M13, Long Gel, 55C, T=6%)

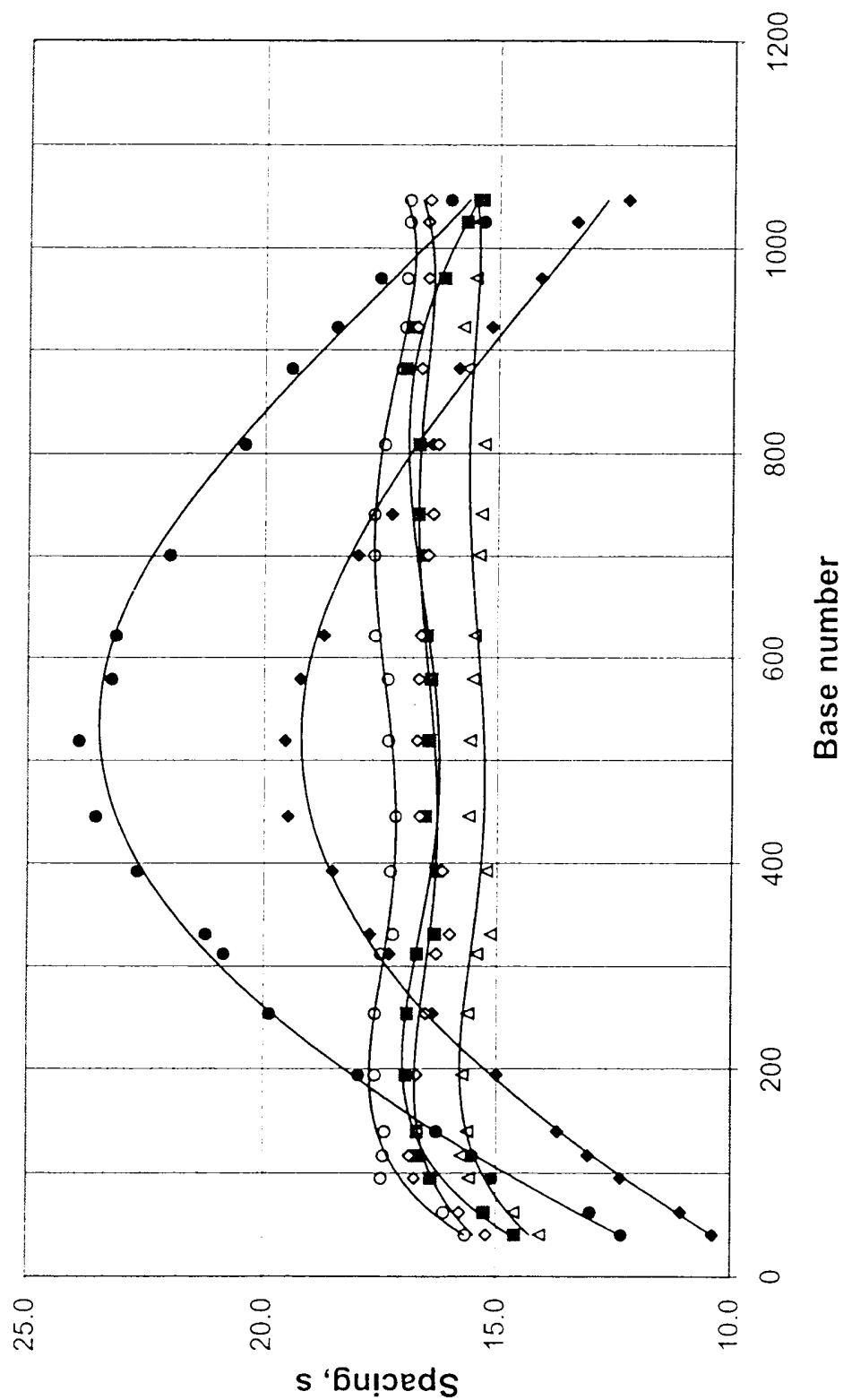


fig. 2

Standard Deviation (%) of the Spacing Between Adjacent Bases from
Average as a Function of Number of Peaks Used as a Reference for
Alignment of Raw Data

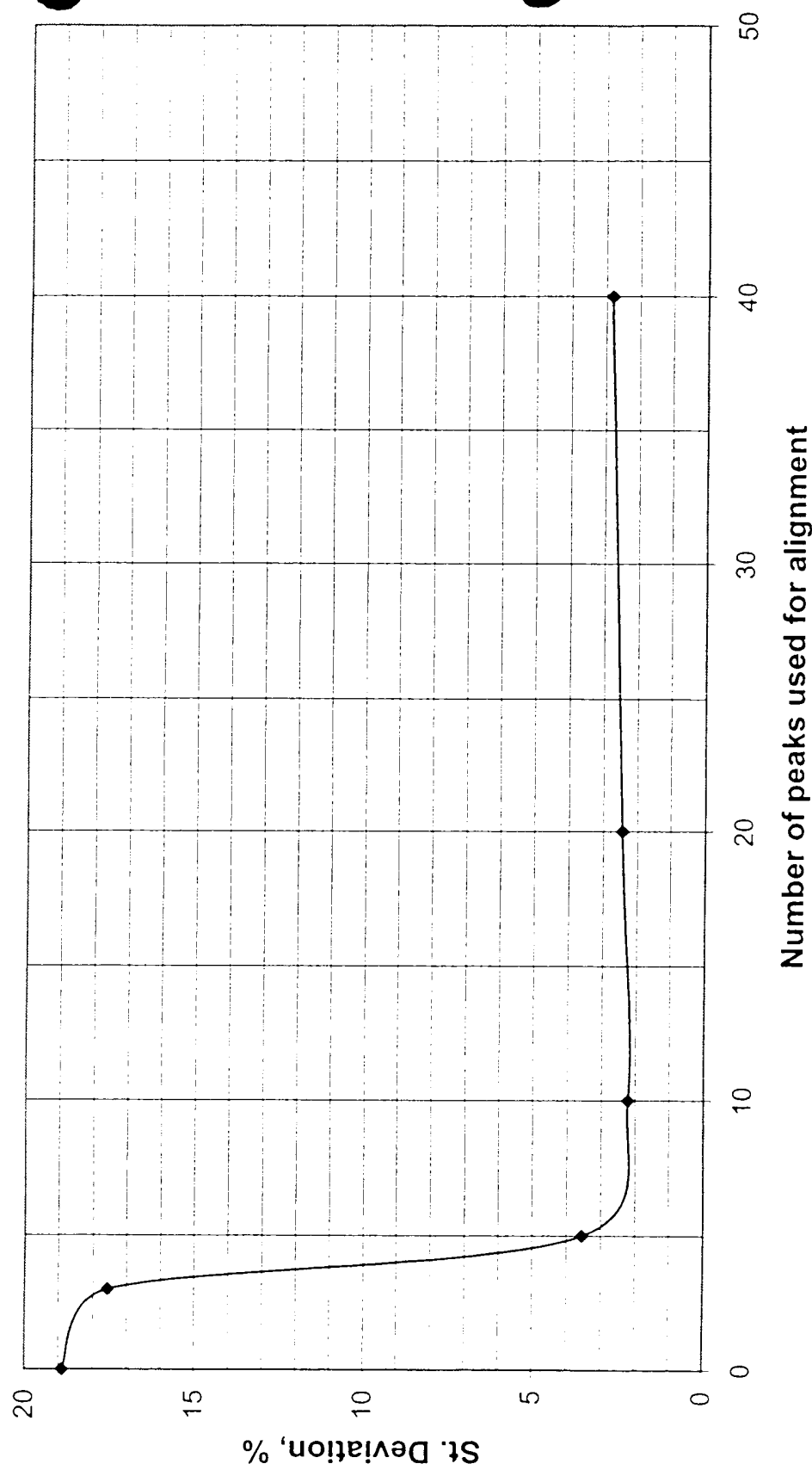


Fig. 3

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Fig. 4

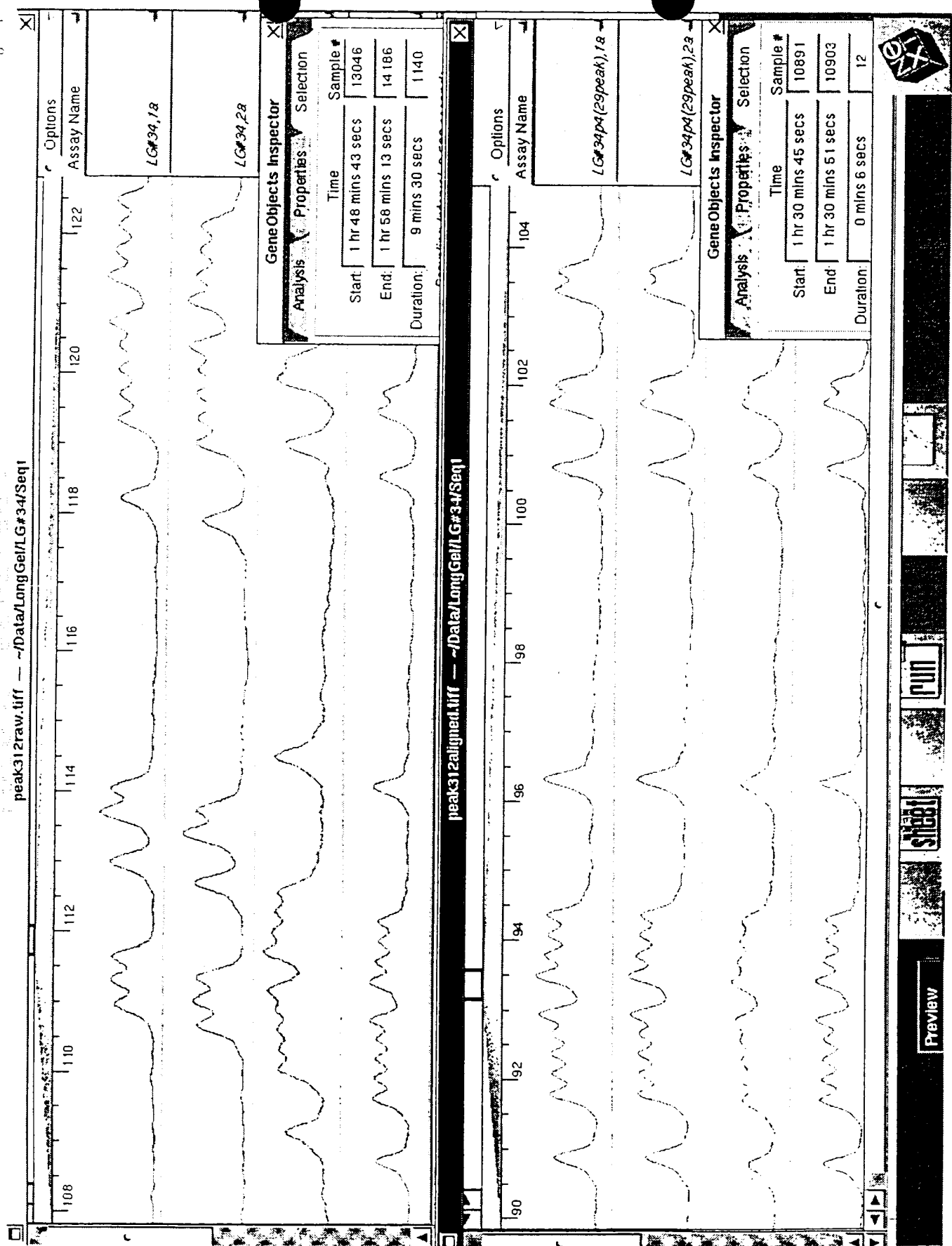
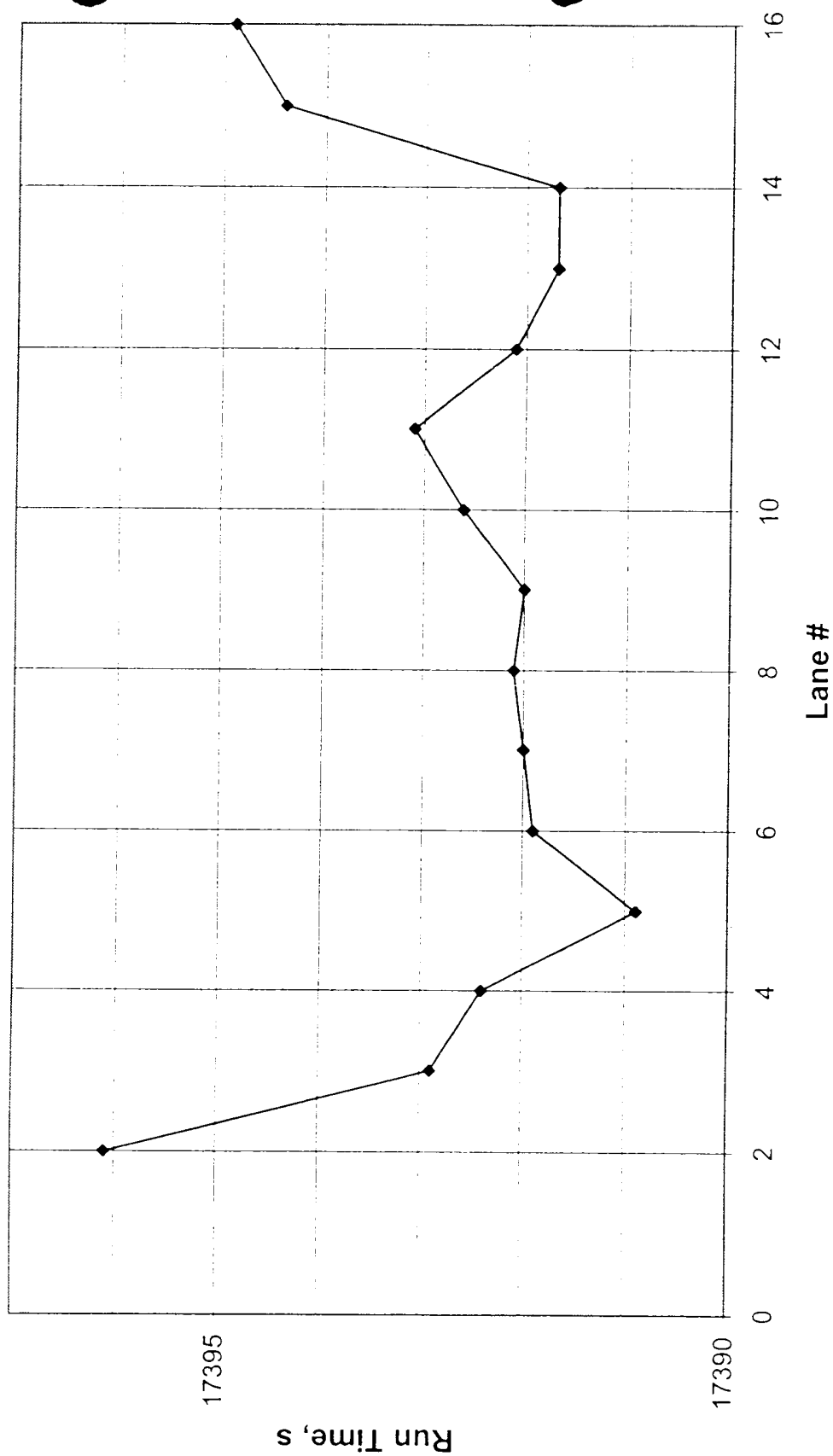


Fig 4

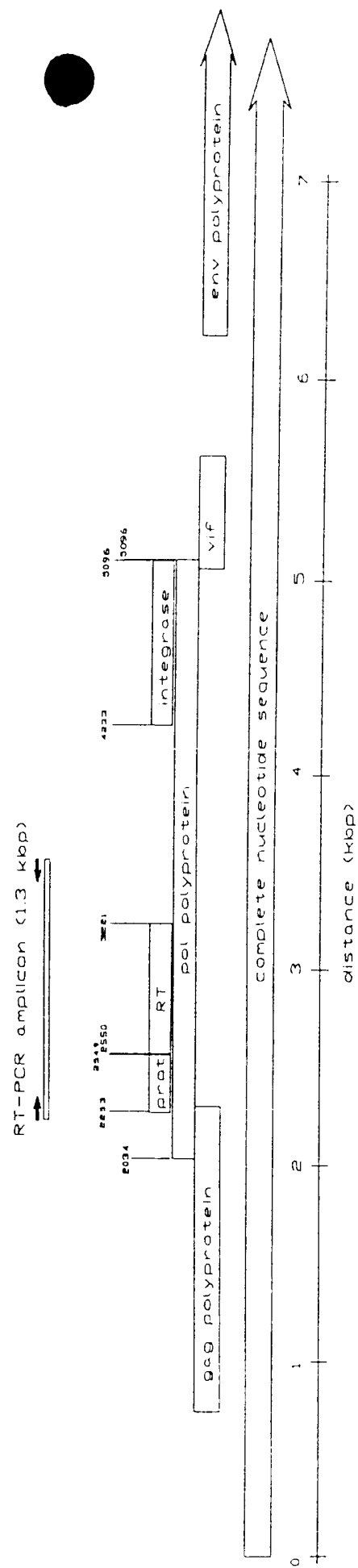
Run Time of the BP#1056 in Different Lanes
(after alignment based on 10 peaks)



h15

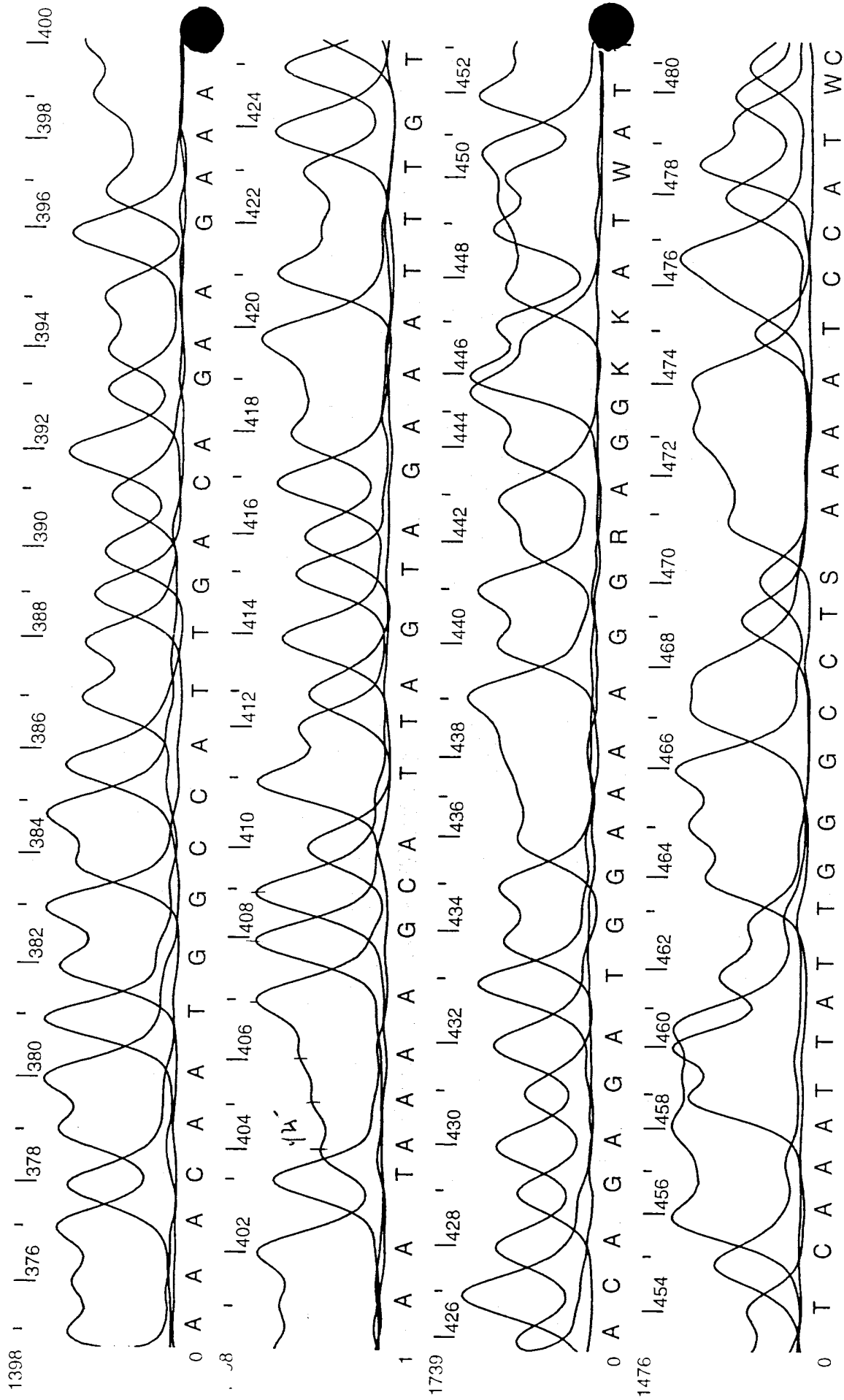
h15

Figure 6

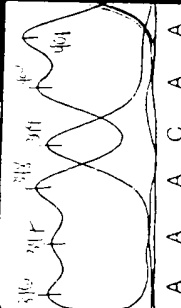


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Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

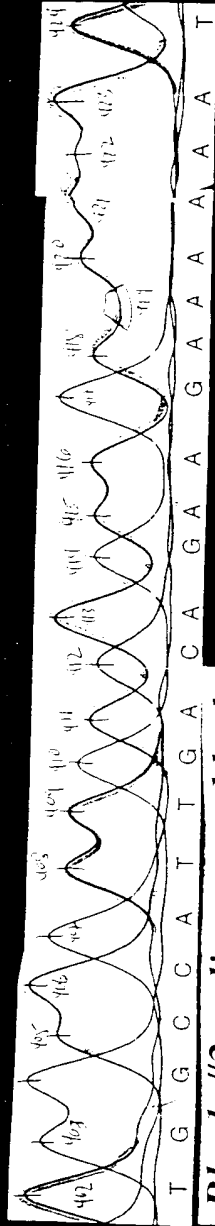


Block #1 -

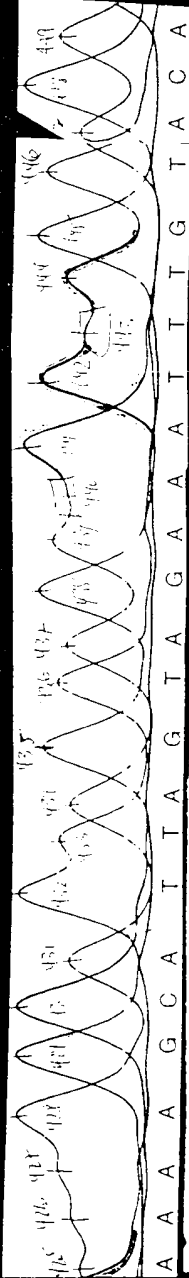


intervening block

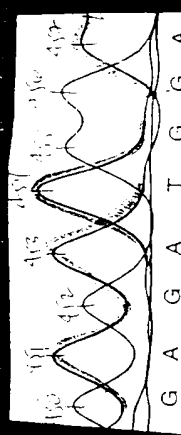
Block #2 - alignment block



Block #3 - intervening block

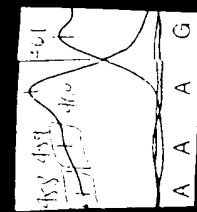


Block #4 - alignment block

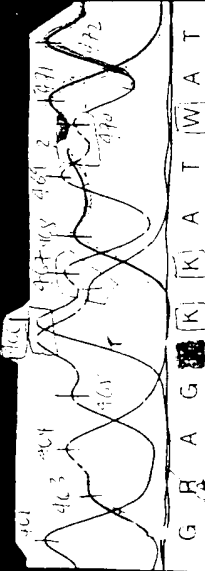


Block #5 -

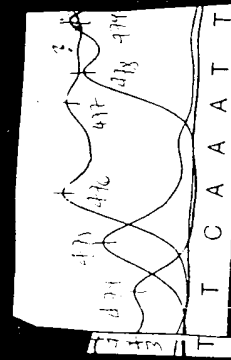
intervening



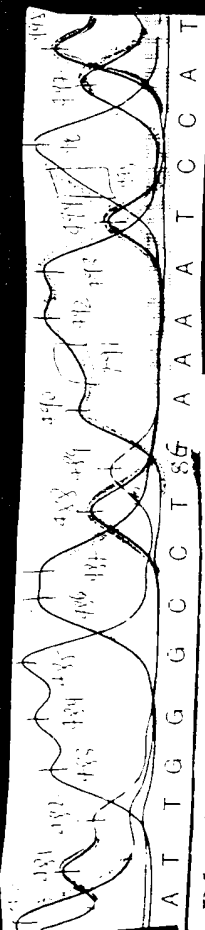
Block #6 - alignment block



Block #7 - intervening block



Block #8 - alignment block



Block #9 - intervening block



Assay Notes. Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc



Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

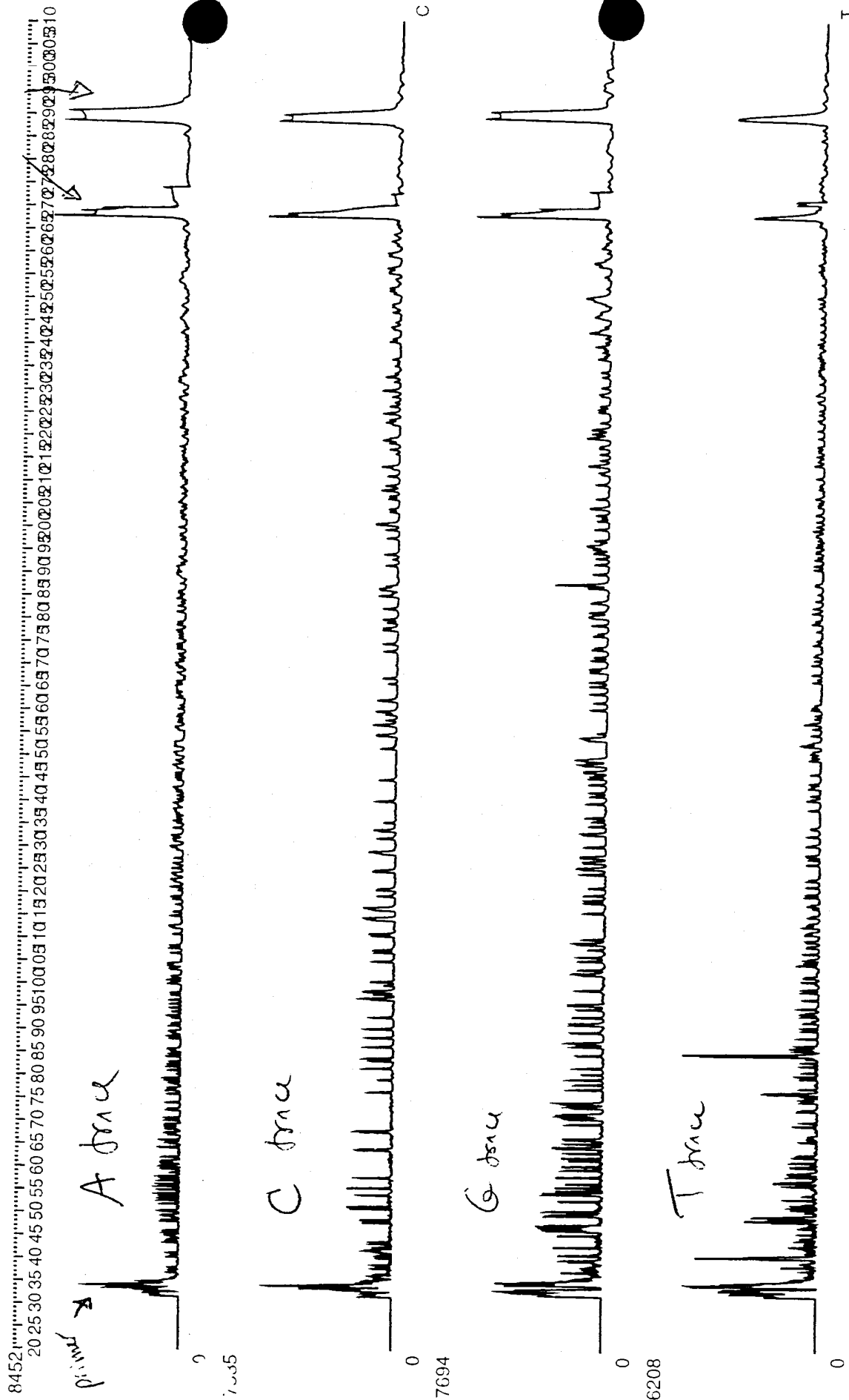


Figure 9A

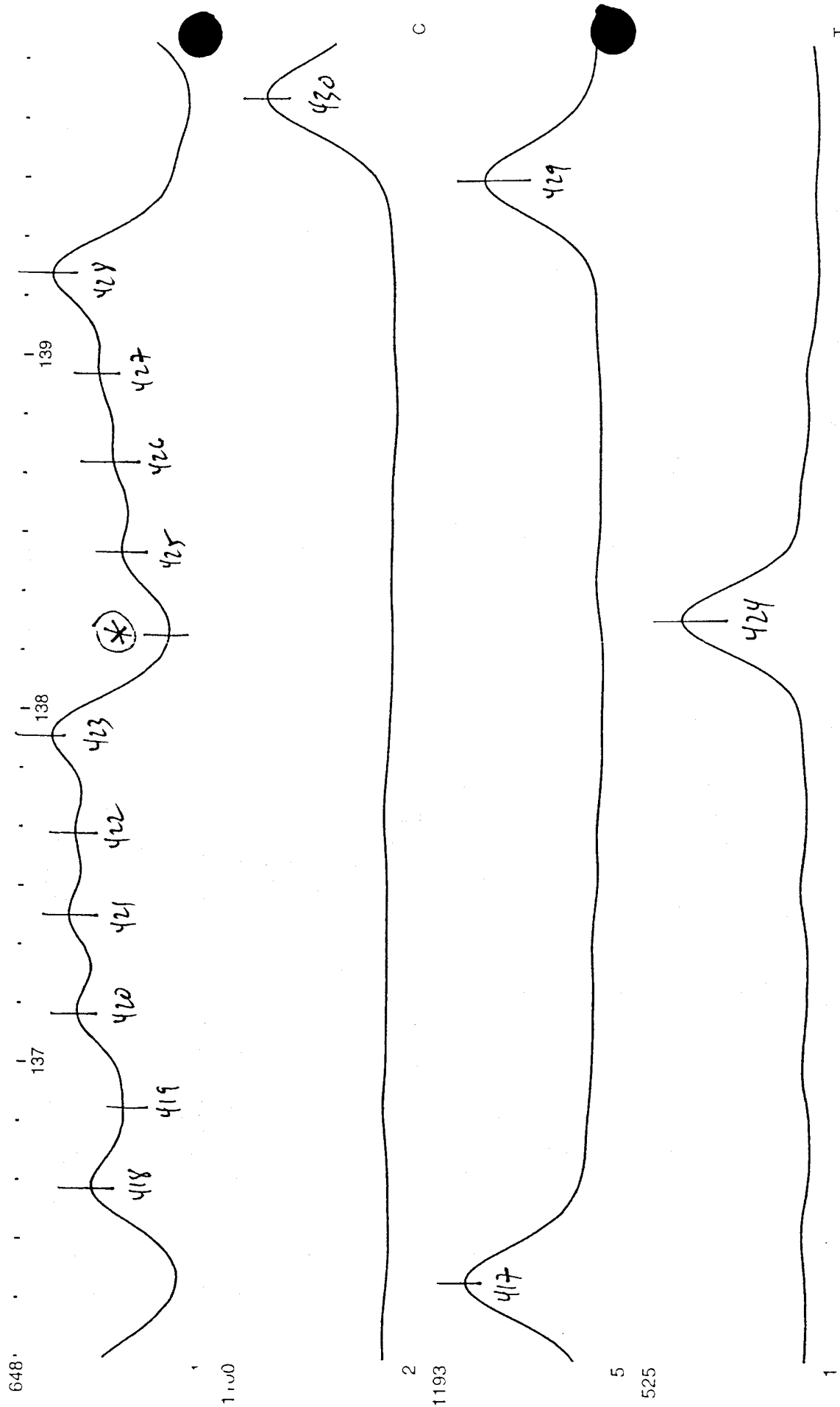


Figure 9B



Assay Notes: Long CLIP with RT-PCR of RNA lyophilized with Glycine+ NaAc

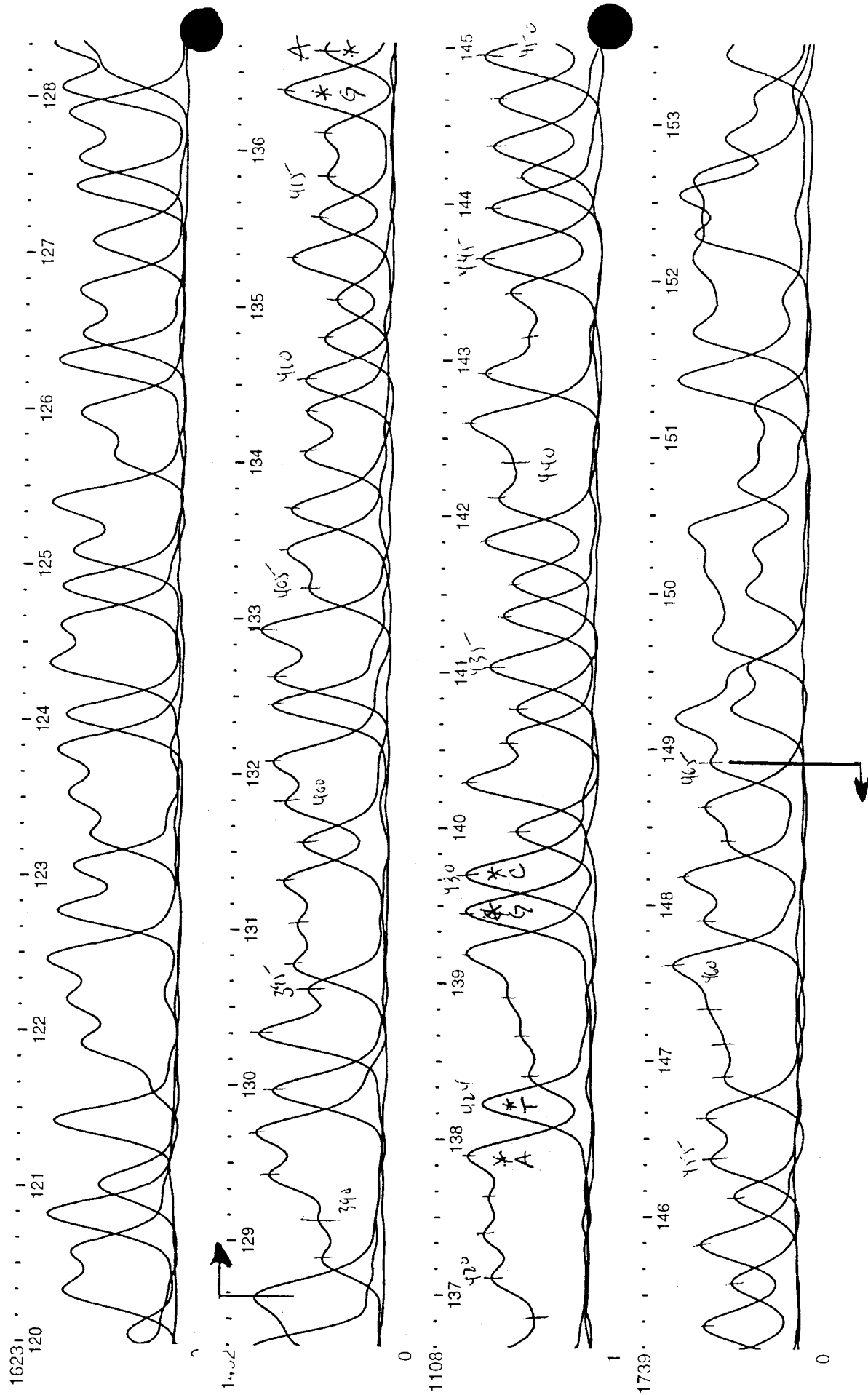


Figure 9a

Deviation of the peak position (in number of bases) from the average
as a function of base number in different traces before alignment

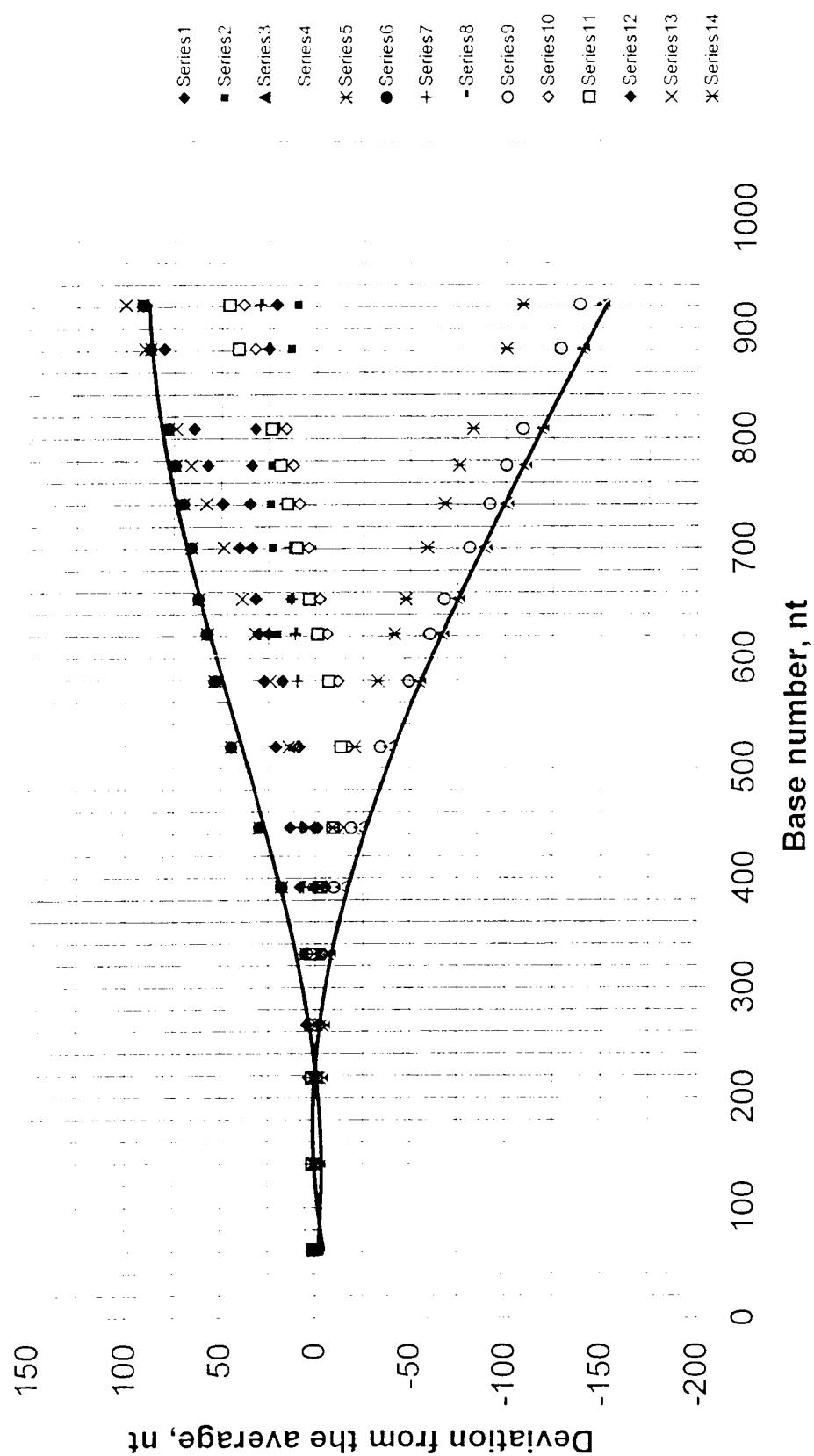


Figure 10

Deviation of the peak position (in number of bases) from the average
as a function of base number in the traces aligned with internal
standards

(long gel, M13, 5-th degree polynomial) 17 ref. peaks

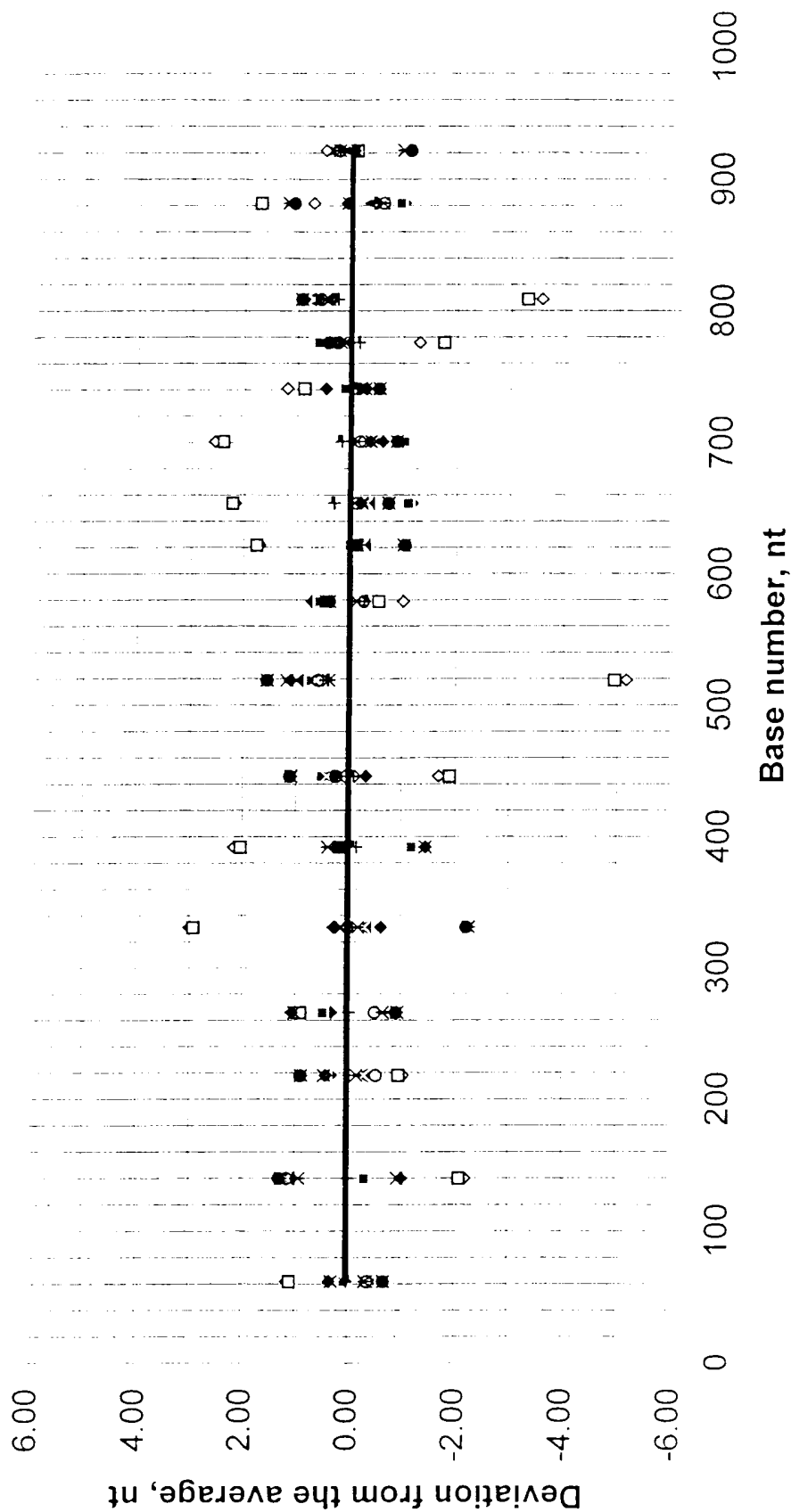


Figure 11

Deviation of the peak position from the average as a function of base number in the traces aligned with internal standards
(long gel, M13, 6 peaks, 5-th degree polynomial)

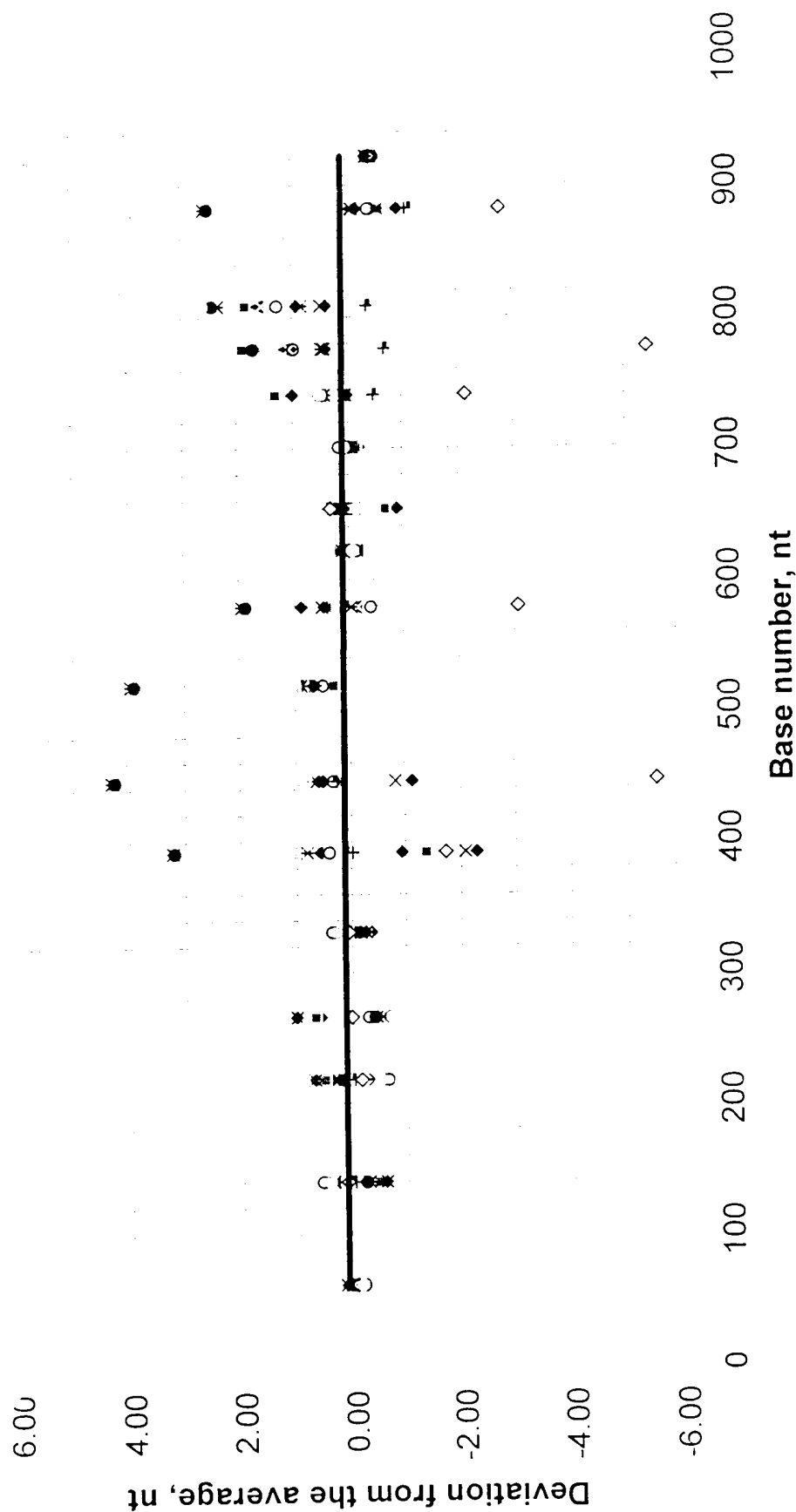


Figure 12